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AIB1 (Amplified in Breast Cancer 1) is a nuclear receptor coactivator found amplified and overexpressed in a subset of breast cancers. AIB1 potentiates the transcriptional activity of the estrogen, progesterone, thyroid hormone, and retinoid receptors. It is necessary for normal female reproductive function and mammary gland development and is rate-limiting for tumor growth in nude mice. It is hypothesized that the amplification and overexpression of AIB1 contribute to the promotion and/or progression of breast cancer. An understanding of the regulation of expression of AIB1 will give insight into the role of AIB1 in breast cancer. This work has shown that antiestrogens, retinoids, and TGF- $\beta$  contribute to the overexpression of AIB1 in MCF-7 breast cancer cells. The putative promoter for the AIB1 gene has been identified. Regulatory elements involved in the regulation of AIB1 by antiestrogens, retinoids, and TGF- $\beta$  were not found in the cloned promoter regions and may be upstream or intronic enhancer elements. Further studies will explore the consequences of overexpression of AIB1 through stable transfection in to a cell line with low endogenous levels of AIB1.

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## INTRODUCTION

AIB1 (Amplified in Breast cancer 1) is a nuclear receptor coactivator found amplified and overexpressed in a subset of breast cancer (1-3). Gene amplification also correlates with estrogen and progesterone receptor positivity of primary breast tumors, as well as with tumor size (3). As a coactivator, AIB1 is able to potentiate the transcriptional activity of the estrogen, progesterone, thyroid hormone, and retinoic acid receptors *in vitro* (1, 2, 4, 5). Disruption of the AIB1 gene results in reduced female reproductive function and blunted mammary gland development in mice (6, 7). Targeted AIB1 reduction in breast cancer cells results in reduced estrogen-dependent colony formation in soft agar and tumor growth in nude mice (8). Based on these findings, AIB1 is an important factor in tumorigenesis. An understanding of the regulation of expression of AIB1 will give insight into the role of AIB1 in cancer. Specifically, the research done with the funding of this grant will identify and examine the regulatory pathways resulting in changes in AIB1 expression levels in response to growth factors, hormones/hormone antagonists, and other relevant agents.

## **BODY**

**Task 1: To identify the factors and mechanisms resulting in increased AIB1 mRNA levels. (Months 1-24)** See appended manuscript reprint.

- a. Analyze the expression levels of AIB1 mRNA in response to hormones, hormone antagonists and other possibly relevant growth factors by Northern blot analysis. (Months 1-6)**
- b. Perform ChIP assays and others to analyze the mechanisms resulting in AIB1 overexpression in response to hormone/hormone antagonists. (Months 7-12)**

The above were completed and addressed in the previous Annual Summary, June 2002.

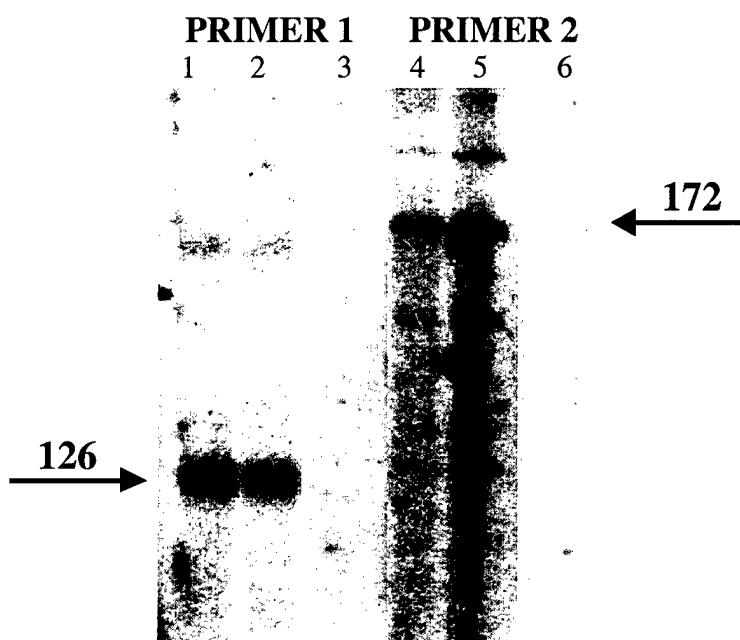
The results were published in *Oncogene* and the reprint is appended.

- c. Obtain/clone the AIB1 gene promoter and begin analysis of regulatory elements. (Months 13-24).**

### **1. Mapping the transcriptional start site of AIB1**

In order to obtain the appropriate genomic sequence it was necessary to first identify the transcription start site, corresponding to the most 5' end of the AIB1 mRNA. Mapping of the transcription start site was carried out by primer extension using mRNA isolated from MCF-7 cells. For primer extension, nested primers were derived from the first and second exon of the 5' untranslated region (UTR) of the known cDNA sequence. Each primer was extended to the 5' end of the AIB1 mRNA transcript, generating a major band of 126 bp

(primer 1) and 172 bp (primer 2) (Figure 1). These bands mapped to a nucleotide position that is 20 nucleotides longer than the originally published sequence for AIB1 (ACTR). (The transcription start site is designated as +1 in the numbering of the genomic promoter sequence (Figure 2).



**Figure 1.** Mapping of the transcription start site of the AIB1 gene. Primer extension of the AIB1 transcript is depicted. The extension reaction was carried out in the presence (lanes 1,2 ,4, 5) or absence (lanes 3, 6) of mRNA isolated from MCF-7 cells. Arrows indicate the size of the band. The transcription start site derived from these results is shown in Figure 2 and is indicated as +1.

**Figure 2**

**AIB1-2.5 →**

CAAGCATGGCTCACTGCAGCCTTGACCTCCCCTACTCAGGCAATCCTCCCACCTCAGCC  
TCCTGAGTACTTGGGAATACAAGCAGGCGCCACCACACCAAGCTAATTTTAAAATTTT  
TG TAGAGACTGGGTATCTGCTTTGTTGCCAAGGCTGGTCTTGAACCTCCTGGGCTCAAGC  
AATCTCTCGGCCTTCCAAAGTGTTGGGATTACAGGCCTGAGCCACTGTGCCCTGGTGGA  
AATATATATATATATATATTTTGTGAGACAGAGTTTCGCTCTTGTGGCCCAGGCTGGAGT  
GCAGTGGCGCGATCTCGGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGTGATTCTCCT  
GCCTCAGCCTCCCGAGTAGCCAGGATTATAGGCGCCTGCCACCATGCCCAGCTAATCTT  
TTGTATTTTAGTAGAGACGGGGTTTCGCCATGTTGGGCAGGCTGGTCTGGAACCTCTG  
ACCTCAGGTGATCTGCCCACCTTGGCCTCCCAAAGTGTTGGGATTACAGGTGTGAGCCA  
CCGTGCCCCGCCCCAGAAATGAGATATTTAATTTTTTAATTTTACTTTTTTTTTTTTG  
AGACGGAGTTTCACTCTTGTTGCCCAGGTTGGAGTGCAATGGTGCCATCTCGGCTCACC  
GCAACCTCTGCCCCCAGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTCGGA  
TTACAGGCATGTGCTACCATGCCCAGCTAATTATGTATTTTAGTAGTGACGGGGTTTC  
TCCATATTGGTCAGGCTGGTCTTGAACCTCCCGACCTCAGGTGATCTGCCTGCCTTGGCC  
TCCCAAAGTGCTGGGATTACATTCGTGAGTCACCGCGCCCAGCCAAAATGAGATATTTT  
AAATAACATAAGTAAACAGAAATATATCATGATTTTAATGATAATTCATGCTCTGAAAA  
TAAATGAAGAAAGGAATAGGAGTAGGGAAAGCTGGGATCAGAGTGGGCAGGAAGTTAAA

**AIB1-1.5 →**

ATAGAGCAGTTAGGGAAAGCCTCACTGAATAAGTGACATTTGGACAATGACCATGGGGA  
GATTAGGGAATGGGTATTTGAATTTTCTGGGAAAATACTGTTCTAGGCAGAGGAAATA  
GCAAGTGCACGATCTTTAAGGCCAGAGTGTGCTAAGCACGTTGGAGAGGCCGAGTCCAT  
TG TAGCTGAGTTACAGAAGTGAGTGGAAGAGAAGAAGGTGATGAGTTTAGAGAGGGAAG  
GGCAGGGCAAGAGACGGGCTGTATGGGGCTTTCAGGTTACTGCAAGAATTTTGCAGGA  
GGGACAGAGACTGACTTGGTTCTTACCAGGATTCCTCTGGCTGCTGTGTTGAGTATAGA

CTCTAAGAGGAAAGAGTGGAAGCAGGCAGAACACTGAGGAGGCTGTTGCAGTGGTCCAG  
 GTGGGAAATGATGGTGCTGACCGTGGAGGTGGTAAGTGGTCAGATTATTCTATTTTATT  
 TACACTCAACACATCTAATACTGACTCAATATTATCTAACATACAGTCCACATTGAAAT  
 TGCCCCCCAAATTCTTTTTACATAAAAAAATCATCCTGAATCCAATCAAGTCTCACCTA  
 TTGCTTTTGGTTTTTACCTCTTTTCATGCTGTCATATTTTAAAAGACTCCAGGCTAGATG  
 TTGTGTAGAATGTCCCACATTCTGAATTCGTTTATTTTTTTCAAGTAAGCTTTTTGTGTG  
 TATGTGGCAAGAATACGACAGAGGTAGCAATATGCTTTCCCCACTGCATCATATTAGGA  
 GACACATAACAACAGTCCTGACCCATTATTGGTGGTGCTAAGTTCGATCACTTGGTAAG  
 GGGGTGCCTGCCAGATCTTCCATTGTAAAGCAAGCTGTTCTTTATTGTAAGTCATAAA  
 TACGCTGTGGGATGATACTTCGGGACTAAATATACCCTGAATATACTGCTGCCCAACAA  
 CATTTACCCAGTGACTTTAGCAGCTAAGGAACAGCCTCGTGGCTTCCGACCTTGTGCC  
 TCAGTTCGCTCATCTGAAAAATGAGGATGATCATGGTCCCTACCGGATGCTTGTTTTGA  
 GGATCCGTGCTTGGCATAACCAGAAACGCTCCACAAATGTTAGGTATTACTGGACGAAGG  
 CAAATATGAAAAAATTAAGGGCAGGGCTAGGACTGCATTCCGGTTCTCCGGATCCCGA  
 GGGAGCTCCCAGTCGATGCTGGGCGAAAGCGGCCGCACGAGCCACGTCGCCACGCCCT  
 CCGCCGCGGAAGCCAGGGTGGGGTTCGCTGGAACCCTAGGCCGGCCGCGCAAGGCCCCC  
 TGGGACCGGTAGTGCTGGGCGTGGCCTCGGGACTACATATCCCAGTGGCCCCCGTGCGG  
 CGACTTTAGCTGCTGTCTCAGCCGCTCCACAG<sup>+1</sup>CGACGGCAGCGGCTGCGGCTTAGT  
 CGGTGGCGGCCGGCGGGCTGCGGGCTGAGCGGCGAGTTTCCGATT

**Figure 2.** Nucleotide sequence of the putative AIB1 promoter. The single strand nucleotide sequence of the AIB1 promoter sequence obtained from Genbank (accession AL35377). The 5' end of the AIB1-1.5 and -2.5 promoter sequences are indicated with



arrows. The nucleotide corresponding to the transcription start site is designated as +1. A potential non-consensus TATA site is located 25 bp upstream and is indicated in BOLD.

## **2. Cloning of the AIB1 promoter**

Isolation and cloning of the AIB1 promoter will allow for analysis of the mechanisms of transcriptional regulation. The identification of the start site of the AIB1 cDNA allows for easy promoter sequence identification. The cDNA sequence of AIB1 (Accession NM\_006534) was compared to the genomic sequence of chromosome 20 using Genome Blast on the NCBI database. The 5' end of the cDNA was located in the genomic sequence (Accession AL353777) and the upstream sequence was identified as the putative AIB1 promoter (Figure 2). A BAC (bacterial artificial chromosome) plasmid with 60 kb of the genomic sequence of chromosome 20 containing the putative promoter of AIB1 and the first exon was obtained from Research Genetics. The cloning strategy is as follows. Briefly, using primers from within the first exon of AIB1 and 1.5 kb and 2.5 kb upstream of this, the putative AIB1 promoter was obtained through PCR using a high fidelity DNA polymerase. These two products were then inserted into a TA cloning vector and then subcloned into the pGL3 luciferase reporter vector. All steps were verified by DNA sequencing analysis.

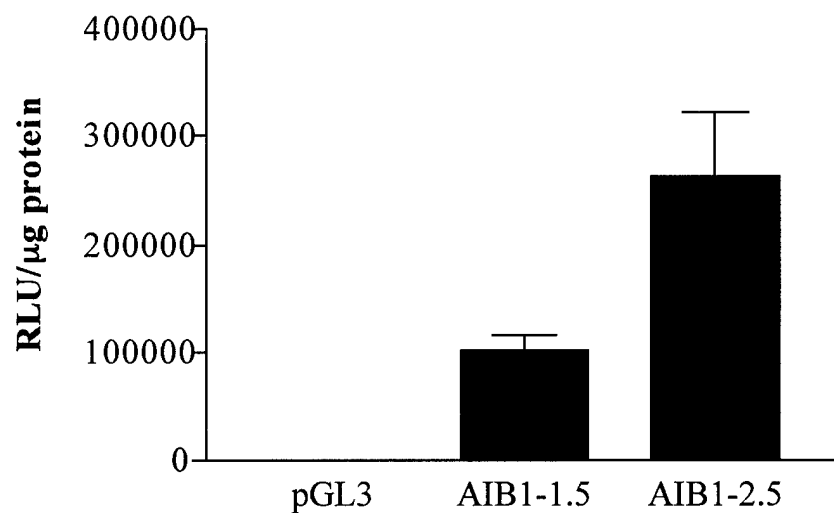
## **3. Sequence analysis of the AIB1 promoter.**

Knowing the transcription start site for the AIB1 mRNA and having identified and isolated the sequence 5' to this region, the sequence was analyzed as the potential promoter for the AIB1 gene. The two sequences were input into the Promoter Finder

database and portions of the sequence were identified as having potential to be promoter sequences. Further analysis of the region directly 5' of the transcription start site did not reveal a consensus TATA box, however a potential non-consensus TATA sequence (TTTA) is located 25 bp upstream of the transcription start site (Figure 2). Sequence analysis of the promoter using the TransFac transcription factor database demonstrated the presence of numerous consensus transcription factor binding sites, indicating potential regulatory elements for AIB1 expression.

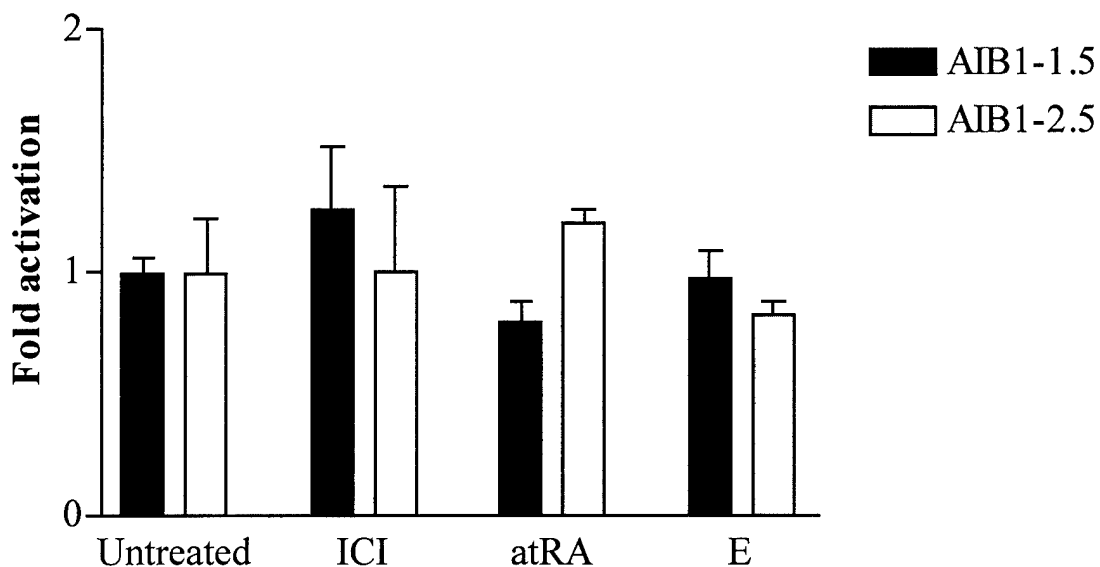
#### **4. Functional analysis of the AIB1 promoter**

In order to test the promoter sequences for activity, the sequences were cloned upstream of a luciferase reporter gene in the promoterless pGL3 basic vector. Using a cationic lipid method, the two putative AIB1 promoters (AIB1-1.5 and AIB1-2.5) were transiently transfected into MCF-7 breast cancer cells and analyzed for their ability to drive luciferase expression. Upon transient transfection of the AIB1-1.5 and AIB1-2.5 promoter/luciferase constructs into MCF-7 cells, luciferase activity was assayed and these constructs were found to drive detectable luciferase expression above background (Figure 3). Luciferase activity of the -2.5 construct was greater than that of the -1.5 construct. Transient transfection of the empty pGL3basic vector resulted in nearly undetectable levels of luciferase expression, suggesting that the sequences in the -1.5 and -2.5 promoter constructs are sufficient to drive AIB1 expression. The increased ability of the -2.5 promoter construct suggests that there are additional positive regulatory elements in this sequence capable of contributing to AIB1 expression.



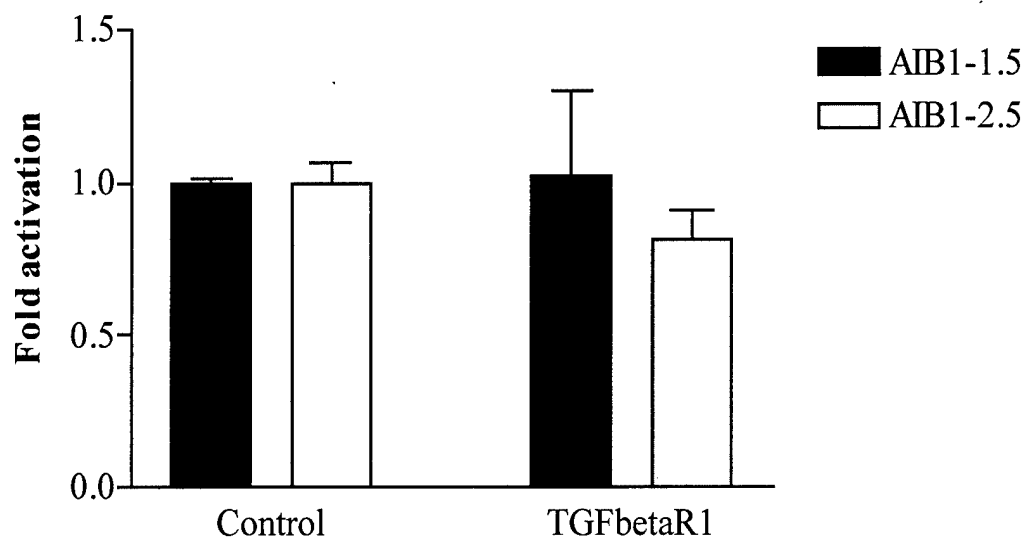
**Figure 3.** The AIB1-1.5 and -2.5 promoter constructs are able to drive luciferase expression. 500 ng of each the AIB1-1.5 and -2.5 promoter constructs along with empty pGL3 vector were transiently transfected into MCF-7 and analyzed for luciferase activity after 24 h. Luciferase activity is expressed as relative light units (rlu) over  $\mu\text{g}$  protein. Error bars indicate SEM and values are representative of at least three experiments performed in triplicate.

In order to determine which elements in the promoter sequence were responsible for the transcriptional regulation of AIB1 by ICI and atRA, seen previously in MCF-7 cells, the -1.5 and -2.5 AIB1 promoter constructs were transiently transfected into MCF-7 cells and treated with estradiol, ICI, or atRA and analyzed for luciferase expression activity. Using various concentrations of promoter/reporter vector, varying times of transfection, as well as in the presence or absence of serum, no significant changes were seen in AIB1 promoter activity of either AIB1.5 or 2.5 kb promoter in response to any of these treatments (Figure 4).



**Figure 4.** The AIB1-1.5 and -2.5 promoter constructs are unaffected by treatment with estrogen, antiestrogen, or retinoids. The AIB1-1.5 and -2.5 promoter constructs were transfected into MCF-7 cells, treated with 10 nM ICI, 10 nM atRA, 10 nM estradiol (E), and the luciferase activity analyzed after 24 h. Untreated/vehicle values were set at 1 and data is expressed as fold activation of treated over untreated/vehicle for each promoter construct. Error bars represent SEM for at least three separate experiments performed in triplicate.

Previously, AIB1 mRNA expression was shown to be upregulated by ICI and atRA through induction of TGF- $\beta$ . Perhaps, the TGF- $\beta$  secretion stimulated by the addition of ICI and atRA in the transient transfection assays was not sufficiently high enough to compensate for the increased concentration of AIB1 promoter in the cells. Therefore, an expression vector containing a constitutively active TGF- $\beta$  receptor was cotransfected with the AIB1-1.5 and -2.5 promoter constructs. Again, no change in AIB1 promoter activity of either promoter construct was detected when compared with the control (Figure 5).



**Figure 5.** Effect of a constitutively active TGF- $\beta$  receptor on AIB1 promoter activity. MCF-7 cells were transiently co-transfected with AIB1-1.5 or -2.5 promoter constructs and a constitutively active TGF- $\beta$  receptor I construct or control and luciferase activity was evaluated. Control values were set at 1 and data is expressed as fold activation of

TGF- $\beta$ RI over control transfection for each promoter construct. Error bars represent SEM for at least three separate experiments performed in triplicate.

The conclusion, therefore, is that while this sequence does contain elements which are able to drive luciferase expression in a transient transfection assay, the sequence(s) responsible for the upregulation of AIB1 expression by ICI, atRA, and TGF- $\beta$  are not present in either the -1.5 or the -2.5 constructs. It is possible that the regulatable sequence(s) of interest lie in intronic enhancer elements or enhancer elements even farther upstream than the cloned region.

**Task 2: Development and phenotypic characterization of cell lines that stably overexpress AIB1. (Months 25-36)**

- a. Transfect breast cancer cell lines with AIB1 and pick clones expressing the highest levels of AIB1 by Northern and Western blot analysis. (Months 25-30)**
- b. Analyze the overexpressing cell lines for changes in rates of proliferation and anchorage independent growth. (Months 31-36)**

For the current grant period, we have tried to make breast cancer cell lines that constitutively overexpress AIB1 or  $\Delta 3$ AIB1 but have invariably lost these clones after several passages. It is possible that this is toxic to the cells or cell growth at high levels and this is why this phenotype is selected against. We have also tried to make stable cell lines that express AIB1-GFP fusion protein. However, in all the cell lines we developed,

although the message was made, AIB1-GFP was cleaved after transfection. To overcome all of the above problems we have now inserted full length tagged AIB1 and  $\Delta 3$ AIB1 into tetracycline regulated vectors. We have made the background MCF-7 + tTA cell line and are now trying to select stable integrants in which we can regulably induce AIB1 or  $\Delta 3$ AIB1 expression. These will then be used in phenotypic and tumorigenic assays.

## KEY RESEARCH ACCOMPLISHMENTS

- Identification of 3 key agents, ICI, RA, and TGF- $\beta$ , that can upregulate AIB1 expression.
- Partial elucidation of the mechanism through which these agents act to upregulate AIB1 expression.
- Identification of the putative AIB1 promoter.
- Regulation of AIB1 mRNA expression by ICI, RA and TGF- $\beta$  does not occur through cloned promoter elements.
- Initiating development of breast cancer cell lines in which we can regulably induce AIB1 or  $\Delta 3$ AIB1 expression.



## REPORTABLE OUTCOMES

**Ph.D.**, granted to **Kristina J. Lauritsen**, May 2003, Department of Tumor Biology, Georgetown University Medical Center, Lombardi Cancer Center, Washington, DC.

“TGF- $\beta$  mediates estrogen and retinoid regulation of the nuclear receptor coactivator AIB1 in MCF-7 breast cancer cells.” **Kristina J. Lauritsen**, Heinz Joachim List, Ronald Reiter, Anton Wellstein, and Anna T. Riegel, *Oncogene*. 2002 Oct 17;21(47):7147-55.

**Lauritsen KJ**, List H-J, Reiter R, Wellstein A, Riegel AT. Estrogen and Retinoid Regulation of the Nuclear Receptor Coactivator AIB1 is Mediated by TGFbeta in MCF-7 Breast Cancer Cells. Era of Hope, Department of Defense Breast Cancer Research Program Meeting, Orlando, FL 2002.

**Lauritsen KJ**, List H-J, Reiter R, Wellstein A, Riegel AT. The Regulation of the Nuclear Receptor Coactivator AIB1 in MCF-7 Breast Cancer Cells. Student Research Days, Lombardi Cancer Center, Georgetown University, Washington, DC 1998-2002.

Invited Lecture, Shippensburg University, Shippensburg, PA. Regulation of AIB1 in Breast Cancer. November, 2002.

## CONCLUSIONS

To date there is limited information on the hormonal or growth factor regulation and expression of the steroid receptor coactivator genes. We have shown, for the first time, the regulation of AIB1 in a human breast cancer cell line, MCF-7. We show that estrogen is able to repress AIB1 gene expression and that AIB1 expression is upregulated following treatment with ICI, OHT, RA, and TGF- $\beta$ . A putative promoter for AIB1 has been identified and cloned however the elements through which ICI, RA and TGF- $\beta$  enact their control over AIB1 mRNA expression are not present within the 2.5 kb of cloned AIB1 gene promoter. It is likely, therefore that an intronic or an upstream enhancer element is responsible for this regulation.

Because AIB1 has been shown to be amplified and overexpressed both in breast tumor tissues and cell lines, as well as rate-limiting in hormone-dependent breast tumor growth, the regulation of AIB1 expression in breast cancer cell lines by antiestrogens and RA has many implications. Suppression of AIB1 by estrogen may be part of a normal reaction to hormone, as a way to dampen or attenuate the response to steroidal stimulation. This normal control may be subverted during antiestrogen therapy, sensitizing the cells to ER or other proliferative signals e.g. through PR or other growth factor stimulated pathways (9). These pathways would not be blocked by antiestrogen therapy and may provoke a tamoxifen/antiestrogen resistant phenotype. Another important consideration is the uterine stimulatory effect of tamoxifen treatment of breast cancer that has been associated with an increased incidence of endometrial cancer. Whether tamoxifen is able to stimulate AIB1 expression in endometrial cells has yet to be shown, but may be an important secondary consideration in breast cancer therapy.

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## A role for TGF- $\beta$ in estrogen and retinoid mediated regulation of the nuclear receptor coactivator AIB1 in MCF-7 breast cancer cells

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**AIB1 (amplified in breast cancer 1) is a nuclear receptor coactivator gene amplified and overexpressed in breast cancer. However, the mechanisms by which AIB1 is regulated are unclear. Here we show that 17 $\beta$ -estradiol represses AIB1 mRNA and protein expression in MCF-7 human breast cancer cells primarily by suppressing AIB1 gene transcription. Estrogen levels present in fetal calf serum are sufficient to maintain AIB1 mRNA and protein at low basal levels, and this repression is reversed by the addition of antiestrogens or all-*trans* retinoic acid. Interestingly, cycloheximide inhibition experiments revealed that secondary protein synthesis was necessary to induce AIB1 expression by antiestrogens and retinoids. Experiments with TGF- $\beta$  and TGF- $\beta$  blocking antibodies demonstrated that this growth factor modulates AIB1 expression and showed that the antiestrogen and retinoid induction of AIB1 gene expression is mediated at least in part through TGF- $\beta$ . These data reveal a mechanism of estrogen-induced down-modulation of the overall hormone sensitivity of cells through feedback inhibition of coactivator gene expression. These data also suggest that antiestrogens can shift the sensitivity of cells to non-estrogenic proliferative signaling by increasing cellular levels of AIB1. This effect may play a role in breast cancer progression and resistance to drug treatment.**

*Oncogene* (2002) **21**, 7147–7155. doi:10.1038/sj.onc.1205943

**Keywords:** AIB1; coactivator; breast cancer; antiestrogen; all-*trans* retinoic acid; TGF- $\beta$

### Introduction

Nuclear hormone receptors are ligand-dependent transcription factors that regulate the expression of genes critical to biological processes such as proliferation, differentiation, development, reproduction, and homeostasis. Recent discoveries have shown that these receptors are often associated with specific cofactors,

corepressors and coactivators, that influence their transcriptional activity (McKenna *et al.*, 1999; McKenna and O'Malley, 2002). In the absence of ligand, some of the nuclear receptors are bound to corepressors such as SMRT and NCoR. After ligand binding, the corepressors are released and nuclear receptor coactivators are recruited. The interaction of the nuclear receptor with its coactivator then leads to enhancement of the transcriptional activity of the nuclear receptors. Some of the best-characterized nuclear receptor coactivators belong to the p160/SRC-family. This family consists of SRC-1, TIF-2/GRIP1 and AIB1/ACTR/RAC3/TRAM-1/SRC-3 (Anzick *et al.*, 1997; Chen *et al.*, 1997a; Guan *et al.*, 1996; Li *et al.*, 1997; Onate *et al.*, 1995; Suen *et al.*, 1998; Takeshita *et al.*, 1997; Voegel *et al.*, 1996; Walfish *et al.*, 1997).

Interestingly, one of these coactivators, AIB1, was found amplified in breast, ovarian, pancreatic, and gastric cancer (Anzick *et al.*, 1997; Ghadimi *et al.*, 1999; Guan *et al.*, 1996; Sakakura *et al.*, 2000). Amplification of the AIB1 gene was correlated with estrogen and progesterone receptor positivity of primary breast tumors as well as with tumor size (Bautista *et al.*, 1998). Independent of any amplification event, increased expression levels of AIB1 also have been found in primary breast tumors (Bouras *et al.*, 2001; Guan *et al.*, 1996; List *et al.*, 2001b). AIB1 enhances the transcriptional activity of the estrogen, progesterone, thyroid hormone, and retinoic acid receptors *in vitro* (Anzick *et al.*, 1997; Chen *et al.*, 1997a; Guan *et al.*, 1996; Li *et al.*, 1997). Cotransfection studies with AIB1 and p53 have shown that AIB1 inhibits p53-dependent transactivation (Lee *et al.*, 1999). Taken together, these findings led to the hypothesis that AIB1 contributes to the development of breast cancer. Furthermore, a recent study demonstrated that disruption of the AIB1 (SRC-3, p/CIP) gene in mice results in a pleiotrophic phenotype where mice display dwarfism, delayed puberty, reduced female reproductive function and blunted mammary gland development (Wang *et al.*, 2000; Xu *et al.*, 2000). AIB1 also seems to play a role in the growth hormone regulatory pathway, as well as in the production of estrogen in mouse development (Wang *et al.*, 2000; Xu *et al.*, 2000). We have recently shown that AIB1 exerts

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a rate-limiting role in hormone-dependent MCF-7 human breast cancer cells (List *et al.*, 2001a). In these studies, reduction of endogenous AIB1, through ribozyme targeting, reduced estrogen-dependent colony formation in soft agar and tumor growth in nude mice (List *et al.*, 2001a).

Based on these findings we were interested in the regulation of AIB1 expression levels by antiestrogens and retinoids, agents that are currently used or tested for breast cancer therapy. In this study, we determined that estrogen can suppress AIB1 gene expression and that antiestrogens and retinoids can reverse this repression. TGF- $\beta$  can also induce AIB1 gene expression and antibody-blocking experiments revealed that a portion of the antiestrogen and retinoid induction of AIB1 mRNA was through secondary induction of TGF- $\beta$  secretion. The opposing regulation of AIB1 gene expression by estrogen, antiestrogens, retinoids, and TGF- $\beta$  has important implications for breast cancer development and therapy.

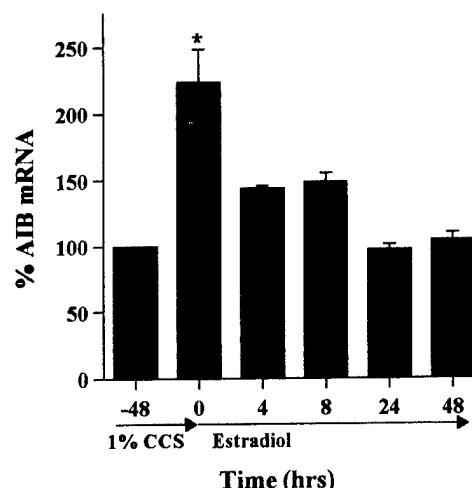
## Results

### Effect of estrogen and antiestrogens on AIB1 gene expression

We observed in a number of experiments with MCF-7 breast cancer cells that serum withdrawal resulted in a significant upregulation of AIB1 mRNA levels. Serum contains sufficient estrogen to produce maximal estrogen responses and these can be blocked by antiestrogens (Lippman and Bolan, 1975). To determine if estrogens directly suppress AIB1 mRNA we kept cells for 48 h in charcoal stripped serum and observed that addition of  $17\beta$ -estradiol reduced AIB1 mRNA levels, with a significant reduction being observed as early as 4 h after the initiation of treatment (Figure 1). In fact, AIB1 mRNA levels were reduced to basal levels (Figure 1) after 24 h exposure to estrogen.

To further investigate if the suppressive effect of serum was through estrogens, we treated cells grown in full serum with additional estrogen and found that no further suppression of the basal levels of AIB1 mRNA in the MCF-7 cells was observed (Figure 2a). This suggests that the estrogen levels in serum are sufficient for full suppression of AIB1 mRNA levels. Consistent with this effect being mediated by estrogens, treatment with the steroidal antiestrogen ICI 182,780 (ICI) resulted in a rapid 2.5-fold induction of AIB1 mRNA levels (Figure 2b). The non-steroidal antiestrogen 4-hydroxytamoxifen (OHT) induced a slightly less than twofold increase in AIB1 mRNA expression (Figure 2c). Finally, we confirmed that induction of AIB1 mRNA by serum withdrawal was the same as antiestrogen treatment since both can be effectively reversed by subsequent treatment with  $17\beta$ -estradiol (compare Figure 1 vs Figure 2d).

The estrogen-mediated repression of AIB1 expression at the mRNA level is paralleled by a reduction in AIB1 protein (Figure 3a). Consistent with this, AIB1



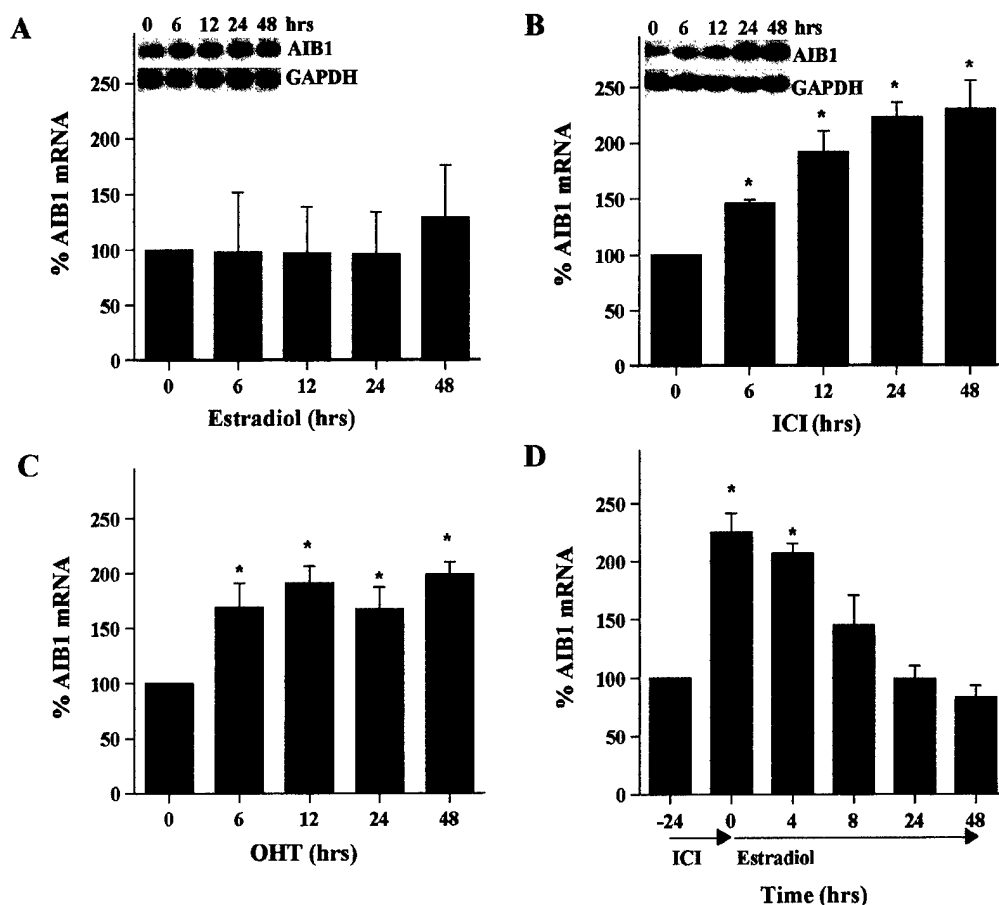
**Figure 1** Effect of estradiol on AIB1 mRNA levels. MCF-7 cells, grown in full serum, were treated with media containing 1% CCS for 48 h followed by  $10^{-7}$  M  $17\beta$ -estradiol. The cytoplasmic RNA was harvested over 48 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated cells (-48 h) were arbitrarily set at 100% and cells treated with hormone in serum free medium were analysed in reference to this. Results are based on three separate experiments performed in duplicate; error bars represent s.e.m. Statistical analyses were performed using a *t*-test. \**P* < 0.05 compared to untreated cells

protein is increased by twofold after antiestrogen treatment of MCF-7 cells (Figure 3b). Interestingly, the hormone and antagonist effects were observed for up to 72 h following treatment. This suggests that sustained changes in AIB1 protein levels are induced after treatment with estrogen or antiestrogen and are not transitory adaptations of the cells to new stimuli.

### Induction of AIB1 gene expression by all-trans retinoic acid

To test if the AIB1 gene is responsive to any other compounds used in the hormonal therapy of breast cancer, we also tested the effect of all-*trans* retinoic acid (atRA), which in some assays antagonizes estrogen effects (Segars *et al.*, 1993). Furthermore, a previous study has shown that atRA is able to induce expression of AIB1 mRNA in another cancer cell line, HL-60 cells, a promyelocytic leukemia cell line (Li and Chen, 1998). We treated MCF-7 cells with atRA in serum-free media for different time periods and found an induction of AIB1 mRNA expression of up to 3.5-fold that begins as early as 6 h after treatment and is maintained for at least 48 h (Figure 4a). Western blot analysis of cells treated with atRA demonstrates an increase of the AIB1 protein (fivefold) that is maintained for at least 72 h after treatment (Figure 4b).

The preceding data suggests that atRA reverses the effect of estrogen suppression and we next wanted to see if this atRA induction, similar to antiestrogens, could be reversed by the addition of estradiol. A



**Figure 2** Effect of 17 $\beta$ -estradiol and antiestrogens on AIB1 mRNA levels. MCF-7 cells, grown in full serum, were treated with serum-free media plus (a) 10<sup>-7</sup> M 17 $\beta$ -estradiol (b) 10<sup>-8</sup> M ICI 182,780 or (c) 10<sup>-6</sup> M OHT. The cytoplasmic RNA was harvested over 48 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Cells shifted from full serum to serum-free medium (0 h) were arbitrarily set at 100% and cells treated with ligands in serum-free medium were analysed in reference to this. Insets represent a typical Northern blot. Results are based on three separate experiments performed in duplicate; error bars represent s.e.m. Statistical analyses were performed using a *t*-test. (a) No significance was found between the data points. (b,c) \**P* < 0.05 compared to untreated cells. (d) MCF-7 cells were treated with 10<sup>-8</sup> M ICI 182,780 for 24 h, washed twice with IMEM followed by treatment with 10<sup>-7</sup> M estradiol. Cytoplasmic RNA was harvested over 48 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated cells (-24 h) were arbitrarily set at 100% and treated cells were analysed in reference to this. Results are based on at least three separate experiments; error bars represent s.e.m. Statistical analyses were performed using a *t*-test. \**P* < 0.05 compared to untreated cells

similar response to the estradiol-mediated repression of the ICI induction of AIB1 mRNA was seen following the induction of AIB1 mRNA by atRA (Figure 4c). In these experiments, estradiol was able to significantly reverse the induction as early as 4 h after treatment, and only slightly more at later time points to levels no longer significantly different from basal.

#### AIB1 regulation is independent of cell cycle regulation

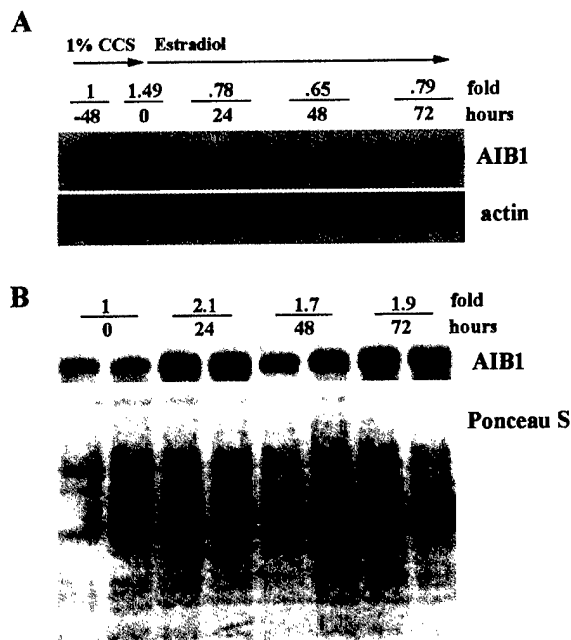
Because antiestrogens and atRA inhibit and estradiol stimulates proliferation of MCF-7 breast cancer cells, we explored the possibility that the induction of AIB1 mRNA in response to these agents might coincide with effects on the cell cycle (Table 1). Examination of the per cent of cells in the S phase vs the G0/G1 phase shows that following 6 h of treatment with each respective agent, a timepoint at which we detected an

**Table 1** Induction of AIB1 is not a result of antiproliferative events in MCF-7 cells

Cell cycle phase	ICI (%)		OHT (%)		atRA (%)	
	S	G0/G1	S	G0/G1	S	G0/G1
Time (h)						
0	45	45	52	27	46	47
6	45	41	37	41	50	37
12	27	57	25	58	35	44
24	6	88	11	76	29	60
48	6	89	23	64	17	72

MCF-7 cells were treated with 10<sup>-8</sup> M ICI, 10<sup>-6</sup> M OHT, and 10<sup>-6</sup> M atRA and harvested for cell cycle analysis over 48 h. Analysis was done by flow cytometry (Materials and methods). Data represent the mean of three separate experiments

increase in AIB1 mRNA levels, there is no concomitant change in the cell cycle status of those cells. Therefore, while the highest levels of AIB1 mRNA



**Figure 3** Estrogen and antiestrogen induced changes in AIB1 protein expression. (a) MCF-7 cells were treated with 1% CCS for 48 h, washed twice with IMEM followed by treatment with  $10^{-7}$  M  $17\beta$ -estradiol. Cell lysates were harvested over 48 h and analysed by Western blot with an anti-AIB1 antibody, stripped and reprobed with anti-actin antibody as a loading control (relative fold changes are shown numerically above lanes). Protein levels were analysed by densitometry. (b) MCF-7 cells were treated with  $10^{-8}$  M ICI 182,780 for 24, 48, and 72 h. Cell lysates were harvested and subjected to Western blot analysis using an anti-AIB1 antibody and staining with *Ponceau S* was used as a loading control (relative fold changes are shown numerically above lanes).

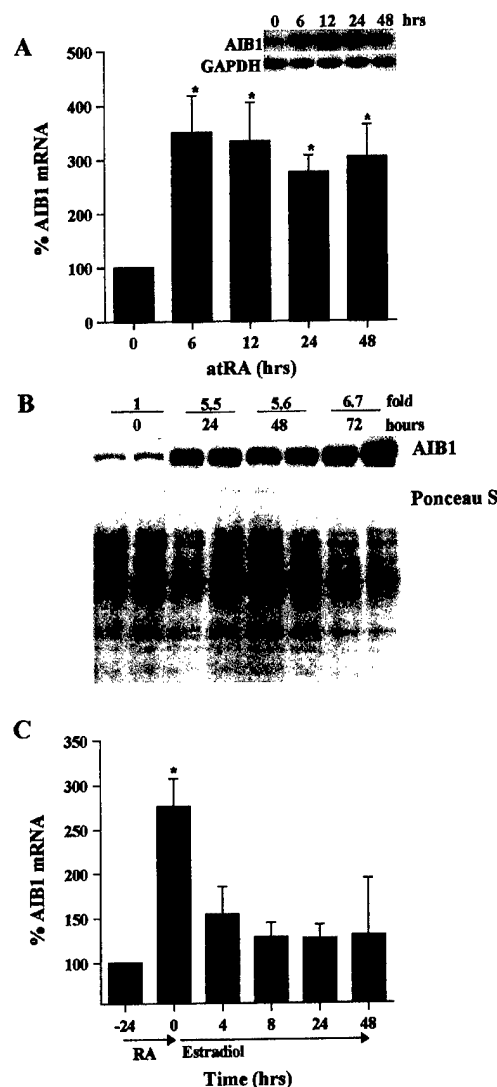
may correlate with the lowest %S and highest %G0/G1, the increased levels of AIB1 during the first 24 h of treatment with each respective agent do not coincide with a decrease in %S or an increase in %G0/G1. Thus, we conclude that the effects of these ligands are directly on AIB1 gene expression rather than indirectly because of proliferative events in the cell.

#### Half-life of AIB1 mRNA is not affected by treatment with $17\beta$ -estradiol, ICI, or atRA

Treatment of MCF-7 cells in serum-free-media in the presence of the transcriptional inhibitor actinomycin D shows an AIB1 mRNA half-life of approximately 4–6 h (Figure 5). There are no significant changes in the half-life of the AIB1 mRNA upon the addition of estradiol, ICI, or atRA indicating that the sustained high levels of AIB1 mRNA in response to ICI and atRA (Figures 2 and 4) are due to an increase of AIB1 transcription rather than a stabilization of the transcript.

#### Antiestrogen induced changes in AIB1 mRNA occur at the transcriptional level

To determine if the increase in AIB1 mRNA is a consequence of direct stimulation of transcription, a

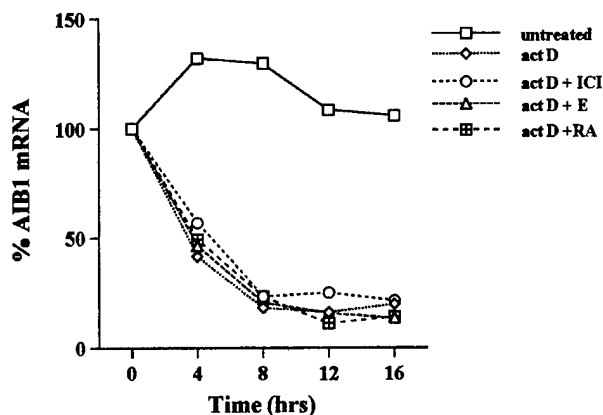


**Figure 4** All-trans retinoic acid increases AIB1 gene expression and is reversed with estradiol. (a) MCF-7 cells were grown in full media for 24 h and then treated with  $10^{-6}$  M atRA in serum-free media and the cytoplasmic RNA was harvested over 48 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated cells (0 h) were arbitrarily set at 100% and treated cells were analysed in reference to this. Results are based on five separate experiments; error represent s.e.m. Statistical analyses were performed using a *t*-test.  $*P < 0.05$  compared to untreated cells. Inset represents a typical Northern blot. (b) MCF-7 cells were grown in full media for 24 h and then treated with  $10^{-6}$  M atRA in serum-free media for 24, 48, and 72 h. Cell lysates were harvested and subjected to Western blot analysis using an anti-AIB1 antibody. *Ponceau S* staining was used as a loading control. Relative fold changes in AIB1 are indicated numerically above lanes. (c) MCF-7 cells were grown in full media and treated with  $10^{-6}$  M atRA in serum-free media for 24 h, washed twice with IMEM followed by treatment with  $10^{-7}$  M  $17\beta$ -estradiol in serum-free media and the cytoplasmic RNA was harvested over 48 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated cells (–24 h) were arbitrarily set at 100% and treated cells were analysed in reference to this. Results are based on at least three separate experiments; error bars represent s.e.m. Statistical analyses were performed using a *t*-test.  $*P < 0.05$  compared to untreated cells. Vehicle control (DMSO and EtOH) showed no statistical difference from untreated cells (data not shown).

chromatin immunoprecipitation (ChIP) assay was performed using an antibody to RNA *PoII* to pull down genes actively undergoing transcription. This allowed us to assay the relative amounts of RNA *PoII* engaged on the AIB1 gene in the ICI-treated vs untreated MCF-7 cells. MCF-7 cells were subjected to the AIB1 suppressive effects of estradiol in serum-free media for 48 h followed by 2 h of ICI treatment in serum-free media. The result demonstrates a significant fourfold increase in transcription of the AIB1 gene following ICI stimulation while cells treated with estrogen had no detectable transcription over background levels when compared with the no antibody control (Figure 6). The lack of effect of estrogen on transcription was expected since the cells had been pretreated for 48 h in serum containing estrogen and basal transcription of AIB1 would be very low under these conditions. While this data demonstrates that the antiestrogen stimulates an increase in transcription (although a transcriptional pause site cannot be ruled out), it does not resolve the question of the mechanism of induction, whether by a direct effect of an antiestrogen-receptor complex on the AIB1 promoter or through induction of a secondary factor that stimulates AIB1 mRNA synthesis.

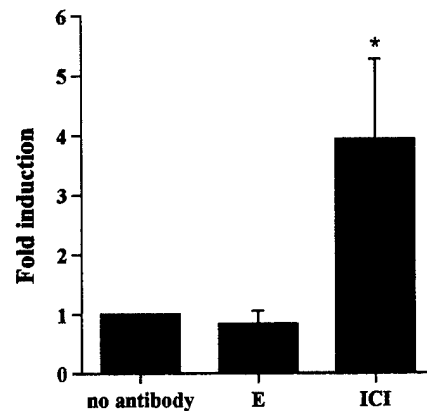
#### *Antiestrogen and retinoid regulation of AIB1 mRNA is partially mediated through TGF- $\beta$*

In order to determine a possible mechanism for the upregulation of AIB1 we studied whether transcriptional stimulation by ICI and atRA requires protein synthesis to stimulate transcription. Treatment of MCF-7 cells with the protein synthesis inhibitor cycloheximide (CHX) in the presence and absence of ICI or atRA demonstrates that protein synthesis is

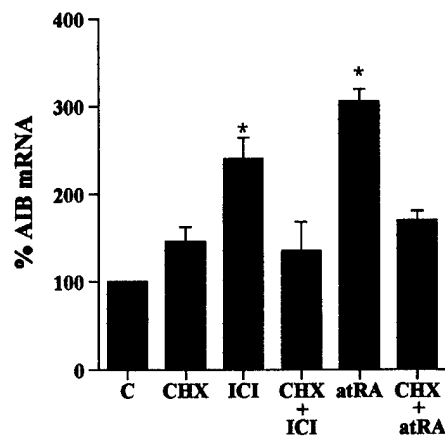


**Figure 5** The half-life of AIB1 mRNA is unaffected by treatment with ICI, atRA, or estradiol. MCF-7 cells were treated with 5  $\mu$ g/ml actinomycin D (act D) alone and in the presence of  $10^{-8}$  M ICI,  $10^{-6}$  M atRA, or  $10^{-7}$  M estradiol and the cytoplasmic RNA was harvested over 16 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated cells at 0 h were arbitrarily set at 100% and treated cells were analysed in reference to this. Results are based on two separate experiments performed in duplicate

necessary for part of the induction of AIB1 transcription by ICI and atRA (Figure 7). A possible candidate protein that might mediate this effect is TGF- $\beta$  since antiestrogens have been shown to directly increase translation and secretion of TGF- $\beta$  in MCF-7 cells



**Figure 6** ChIP assay demonstrates increased transcription following stimulation by ICI. MCF-7 cells were treated for 48 h with  $10^{-7}$  M  $17\beta$ -estradiol in the absence of serum. Cells were washed twice with IMEM and stimulated for 2 h with  $10^{-8}$  M ICI. An antibody to RNA *PoII* was used for immunoprecipitation and a fragment of AIB1 exon 4 was amplified and quantified by real time PCR. The amount of AIB1 DNA pulled down by IP was corrected for the amount of DNA in the input. The no antibody control indicates background levels of AIB1 pulled down non-specifically during IP and was arbitrarily set at 1. The amount of AIB1 DNA pulled down in the estradiol and ICI treated cells is expressed as fold induction over the background no antibody control. Results are based on at least three separate experiments; error bars represent s.e.m. Statistical analyses were performed using a *t*-test. \**P* < 0.05 compared to untreated cells



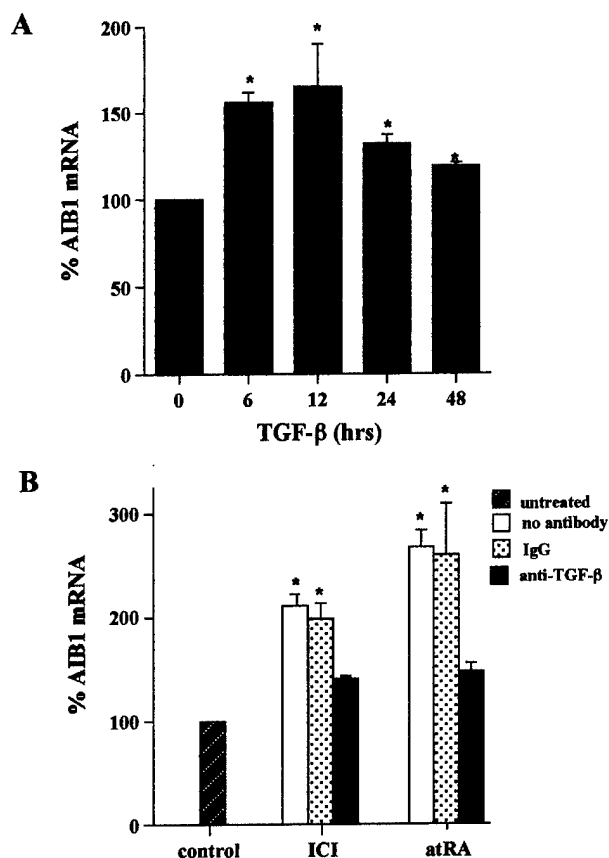
**Figure 7** *De novo* protein synthesis is necessary for the induction of AIB1 mRNA by ICI and atRA. MCF-7 cells were treated with 10  $\mu$ g/ml cycloheximide (CHX) alone and in the presence of  $10^{-8}$  M ICI or  $10^{-6}$  M atRA and the cytoplasmic RNA was harvested after 24 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated control cells (C) were arbitrarily set at 100% and treated cells were analysed in reference to this. Results are based on at least three separate experiments; error bars represent s.e.m. Statistical analyses were performed using a *t*-test. \**P* < 0.05 compared to untreated cells



(Knabbe *et al.*, 1987). Interestingly, in the A549 lung carcinoma cell line, TGF- $\beta$  was able to induce an increase in AIB1 levels (Akiyama *et al.*, 2000). In addition, other studies support a role for atRA in the production of TGF- $\beta$  (Choudhury *et al.*, 2000; Degitz *et al.*, 1998; Jakowlew *et al.*, 2000). Therefore, we postulated that if TGF- $\beta$  is able to effect an increase in AIB1 mRNA in MCF-7 cells, then the induction by ICI, OHT and atRA might be a result of stimulation of TGF- $\beta$ , which in turn induces AIB1 mRNA. To examine this, we first treated MCF-7 cells with a single dose of TGF- $\beta$  and found that it is able to increase AIB1 mRNA levels 1.6-fold 12 h after treatment, with mRNA levels returning to basal values 48 h after treatment (Figure 8a). Because TGF- $\beta$  was able to produce an induction of AIB1 mRNA levels, we next tested the hypothesis that the induction by ICI and atRA is mediated through a TGF- $\beta$  increase. For this, we treated MCF-7 cells for 24 h with ICI and atRA with or without a TGF- $\beta$  blocking antibody. The blocking antibody prevented most of the induction of AIB1 mRNA by both ICI and atRA, demonstrating that TGF- $\beta$  contributes to the induction of AIB1 mRNA by ICI and atRA (Figure 8b).

## Discussion

To date there is limited information on the hormonal or growth factor regulation and expression of the steroid receptor coactivator genes. SRC-1, the first member of the SRC family, was shown to be upregulated in GH3 rat pituitary cells by thyroid hormone, as well as a small *in vivo* induction in the rat pituitary gland (Misiti *et al.*, 1998). Conversely, SRC-1 mRNA was downregulated in GH3 cells and in *in vivo* studies by the administration of estradiol (Misiti *et al.*, 1998). AIB1 (RAC3) has been previously described to be regulated by atRA in HL60 and NB4 promyelocytic leukemia cell lines resulting in significant enhancement of AIB1 mRNA expression (Li and Chen, 1998). Using gene trapping in A549 human lung carcinoma cells AIB1 was described as one of a number of TGF- $\beta$  responsive genes in these cells showing a small upregulation of expression (Akiyama *et al.*, 2000). Alternately, *in vivo* studies of rat uteri following treatment with estradiol and OHT showed no alteration of expression of any coactivators of the SRC family, including AIB1 (Nephew *et al.*, 2000). In the present study we show, for the first time, regulation of AIB1 mRNA expression in a human breast cancer cell line, MCF-7. We show that estrogens can suppress AIB1 gene expression, and report an upregulation of AIB1 following treatment with the antiestrogens ICI and OHT, as well as with atRA and TGF- $\beta$ . In addition we demonstrate that estradiol present in serum is sufficient to repress the basal levels of AIB1 mRNA and that this suppression can be reversed by ICI and atRA. We propose that this feedback loop is one physiological mechanism whereby cells modulate the



**Figure 8** ICI and atRA act through TGF- $\beta$  to increase AIB1 mRNA levels. (a) MCF-7 cells grown in full media for 24 h and were treated with 10 ng/ml TGF- $\beta$  in serum-free media and the cytoplasmic RNA was harvested over 48 h. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated cells (0 h) were arbitrarily set at 100% and treated cells were analysed in reference to this. Results are based on at least three separate experiments. Statistical analyses were performed using a *t*-test. \**P* < 0.05 compared to untreated cells. (b) MCF-7 cells were grown in full media for 24 h and treated with  $10^{-8}$  M ICI or  $10^{-6}$  M atRA for 2 h in serum-free media, then 50  $\mu$ g/ml anti-TGF- $\beta$  or control antibody (normal chicken IgY) was added to the media and the cytoplasmic RNA was harvested 24 h later. Following Northern blot analysis, AIB1 levels were analysed by phosphorimager and corrected by GAPDH. Untreated cells (control - 0 h) were arbitrarily set at 100% and treated cells were analysed in reference to this. Results are based on one experiment performed in triplicate. Statistical analyses were performed using a *t*-test. \**P* < 0.05 compared to untreated cells

overall estrogenic signaling by regulation of a coactivator that is required for hormone regulation of a number of cellular genes.

AIB1 has been shown to be amplified and over-expressed in both breast tumor tissue and cell lines, and is also rate-limiting in hormone-dependent breast tumor growth. We have now shown, in the breast cancer cell line MCF-7, that the expression of AIB1 mRNA can be hormonally regulated. AIB1 has coactivator functions in conjunction with nuclear receptors, the TEF family of transcription factors (Belandia and Parker, 2000), as well as with p53 (Lee *et al.*, 1999) that are only now being elucidated. As

such, the regulation of AIB1 expression in breast cancer cells by antiestrogens and atRA has many implications. The suppression of AIB1 by estrogen may be a normal reaction to hormone stimulation, a way of dampening or attenuating the response to steroidal stimulation and this normal control may be subverted during antiestrogen therapy. In its function as a coactivator of the estrogen receptor, upregulation of AIB1 may serve to increase sensitivity to low levels of ER and pave the way for eventual tamoxifen resistance seen in many breast cancers. Increasing AIB1 levels would either make the ER over-sensitive to stimulation or would sensitize the cell to other proliferative signals e.g. through PR or growth factor stimulated pathways (Reiter *et al.*, 2001; Xu *et al.*, 2000). These pathways would not be blocked by antiestrogen therapy. In addition, while it is commonly believed that through its antiestrogen-induced upregulation, TGF- $\beta$  acts as a mediator of growth inhibition by tamoxifen, there is evidence to support a role for TGF- $\beta$  independent of tamoxifen (Karey and Sirbasku, 1988; Koli *et al.*, 1997). There is also evidence to suggest that TGF- $\beta$  may play a role in the stimulation of invasiveness and metastasis of cancer cells (Dumont and Arteaga, 2000; Farina *et al.*, 1998; Oft *et al.*, 1998; Welch *et al.*, 1990). Taken together these data indicate a possible role for AIB1 in development of tamoxifen resistance and invasiveness of breast cancer cells. And in fact, Taiman, a *Drosophila* homolog to AIB1, is required for cell motility indicating a role in stimulation of invasive cell behavior (Bai *et al.*, 2001).

Conversely, in its role as a coactivator of other nuclear receptors, upregulation of AIB1 by antiestrogens, atRA, or through TGF- $\beta$  may serve as a cellular defense mechanism to the antiproliferative properties of these agents by enhancing the transcriptional activity of nuclear receptors. Another important consideration is that the uterine stimulatory effect of tamoxifen treatment in breast cancer has been associated with an increased incidence of endometrial cancer. Whether tamoxifen is able to stimulate an increase in AIB1 in human endometrial cells has yet to be shown, but may be an important secondary consideration in breast cancer therapy. Interestingly, because AIB1 is known to coactivate the RAR and RXR (Chen *et al.*, 1997b), this upregulation is suggestive of an autoregulatory event where, in contrast to the ER negative feedback, AIB1 is continuously transcribed to ensure continuous transactivation by RAR and RXR. In both these systems it appears that AIB1 levels would be an important set point determinant of the extent of signaling through estrogens or retinoids.

## Materials and methods

### Cell culture and reagents

The human breast cancer cell line MCF-7 was cultured in modified improved minimal essential medium (IMEM) containing L-glutamine (Life Technologies, Inc.) with 10% fetal bovine serum (Life Technologies, Inc.). ICI 182,780

(ICI), 17 $\beta$ -estradiol, and 4-hydroxytamoxifen (OHT) were dissolved in ethanol, all-trans retinoic (atRA) acid was dissolved in dimethyl sulfoxide (DMSO). Recombinant human transforming growth factor  $\beta$ -1 (TGF- $\beta$ -1) was obtained from Life Technologies, Inc. and dissolved in water and a monoclonal antibody to TGF- $\beta$ -1,2,3 was obtained from R&D Systems. These reagents were used at concentrations used by others in similar cell systems (Wang *et al.*, 1999; Reiter *et al.*, 2001; List *et al.*, 2001a; Yue and Mulder, 2000).

### Cytoplasmic RNA preparation

MCF-7 cells were grown for 24 h in 15 cm dishes to 75% confluence in IMEM containing 10% fetal calf serum. Following this, cells were washed twice in serum-free IMEM, and treated with the indicated drug in serum-free IMEM. Cells, treated with ICI ( $10^{-8}$  M) or atRA ( $10^{-6}$  M) for 24 h before treatment with estradiol were washed twice in serum-free IMEM before estradiol treatment. Cytoplasmic RNA was isolated by scraping and collecting the cells in cold  $1 \times$  PBS. Lysis buffer (0.2 M Tris-HCl, pH 8.0, 0.14 M NaCl, 2 mM MgCl<sub>2</sub>, 0.5% Nonidet P-40) was added to resuspend pelleted cells on ice for 4 min. Nuclei were pelleted by a 15 s spin (14000 g) and the supernatant transferred to a tube containing 0.5 ml phenol:chloroform:isoamyl alcohol (25:24:1 wt/vol) (PCI) (Life Technologies, Inc.) and 0.5 ml STE (5 mM Tris-HCl, pH 8.5, 2 mM EDTA, 0.2% SDS). Samples were vortexed and spun (14000 g) in an eppendorf centrifuge for 15 min at room temperature. The aqueous layer was removed to a new tube containing 0.5 ml PCI and the extraction was repeated. RNA was precipitated overnight at  $-20^{\circ}\text{C}$  in an equal volume of ethanol.

### Northern blot analysis

Fifteen  $\mu\text{g}$  of cytoplasmic RNA were separated by electrophoresis in a 1.2% formaldehyde-agarose gel. The gel was soaked for 5 min in 0.1N NaOH, for 30 min in  $20 \times$  SSC (0.9 M sodium chloride, 0.09 M sodium citrate, pH 7.0) and then blotted onto a nylon transfer membrane (Osmonics, Inc.). The blots were prehybridized in  $6 \times$  SSC, 0.5% (wt/vol) SDS,  $5 \times$  Denhardt's solution (0.1% (wt/vol) Ficoll, 0.1% (wt/vol) polyvinylpyrrolidone, 0.1% (wt/vol) bovine serum albumin, 100  $\mu\text{g}/\text{ml}$  sonicated salmon sperm DNA) (Life Technologies, Inc.) for 4 h at  $42^{\circ}\text{C}$ . Hybridization was carried out overnight at  $42^{\circ}\text{C}$  in the same buffer. After hybridization, blots were washed three times with  $2 \times$  SSC/0.1% SDS for 5 min at  $42^{\circ}\text{C}$ , once with  $1 \times$  SSC/0.1% SDS for 10 min at  $42^{\circ}\text{C}$ , and with  $0.1 \times$  SSC/0.1% SDS for 10 min at  $42^{\circ}\text{C}$ . Hybridization probes were prepared by random-primed DNA labeling (Amersham Pharmacia Biotech) of AIB1 and human GAPDH (Clontech). The AIB1 probe is a 7.5 kb EcoRI-fragment from pCMX-ACTR A38, encompassing amino acids 703–927 of AIB1 (Chen *et al.*, 1997a). Quantitation of mRNA levels was performed using a PhosphorImager (Molecular Dynamics).

### Cell cycle analysis

MCF-7 cells were grown for 24 h in 10 cm dishes to 75% confluence, washed twice in serum-free IMEM, and treated with the indicated drug in serum-free IMEM. Cells were harvested using trypsin (Life Technologies) and verified microscopically to be in a single cell suspension. The cell number was adjusted to  $1-2 \times 10^6$  cells per tube and centrifuged (1000 g) for 5 min. The supernatant was removed and cells were resuspended in 100  $\mu\text{l}$  of citrate/DMSO buffer

and transferred to polystyrene tubes (Falcon). Cells were frozen immediately in dry ice and stored at  $-80^{\circ}\text{C}$ . Cell cycle analysis was performed by Vindelov staining using a flow cytometer (Vindelov *et al.*, 1983).

#### Western blot analysis

MCF-7 cells were grown for 24 h in 10 cm dishes to 75% confluence, washed twice in serum-free IMEM, and treated with the indicated drug in serum-free IMEM. Cells were washed with  $1\times$  PBS, harvested with a cell scraper, and washed twice with wash buffer (10 mM HEPES, pH 7.8, 1.5 mM  $\text{MgCl}_2$ , 10 mM KCl, 0.5 mM dithiothreitol, protease inhibitor mixture (Complete<sup>TM</sup>, Roche Molecular Biochemicals)). The cell pellet was resuspended in lysis buffer (20 mM HEPES, pH 7.8, 1.5 mM  $\text{MgCl}_2$ , 420 mM NaCl, 25% (v/v) glycerol, 0.2 mM EDTA, 0.5 mM dithiothreitol, protease inhibitor mixture, 0.1% Nonidet P-40) and incubated for 10 min on ice. The suspension was centrifuged at  $14\,000\text{ g}$  at  $4^{\circ}\text{C}$  for 10 min. Forty  $\mu\text{g}$  of supernatant protein were electrophoresed on a 4–20% SDS-polyacrylamide gel. After electrophoresis, the proteins were transferred to a nitrocellulose membrane, and the membrane was incubated for 1 h at room temperature with 5% nonfat milk in PBST (PBS, 0.5% Tween 20) followed by washing four times for 5 min each with PBST. The membrane was incubated for 1 h at room temperature with primary anti-AIB1 antibody (Transduction Laboratories), washed as described above, and incubated for 1 h with a secondary antibody-peroxidase conjugate (10 000-fold dilution in PBST). After washing, the membranes were incubated for 1 min with ECL detection solution (Amersham Pharmacia Biotech) and then exposed to film. Bands were quantitated using densitometry.

#### Formaldehyde crosslinking and chromatin immunoprecipitation (ChIP assay)

MCF-7 cells were grown in 15 cm dishes to approximately 50% confluence, washed twice with serum-free IMEM and treated for 48 h with  $10^{-7}\text{ M}$  estradiol in IMEM. Cells were then washed twice with serum-free IMEM and treated for 2 h with  $10^{-8}\text{ M}$  ICI 182 780. Proteins were crosslinked to DNA by adding formaldehyde directly to the culture medium to a final concentration of 1%. Cells were incubated 15 min at room temperature, washed, and scraped into 1 ml  $1\times$  PBS

containing  $1\times$  protease inhibitor cocktail (Complete<sup>TM</sup>, Roche Molecular Biochemicals). Cell pellets were lysed in 200  $\mu\text{l}$  lysis buffer (1% SDS, 10 mM EDTA, 50 mM Tris-HCl, pH 8.0,  $1\times$  protease inhibitor cocktail) for 10 min on ice. Lysates were sonicated on ice to an average length of 200 to 600 bp and centrifuged to remove cell debris. Supernatant was diluted fivefold in immunoprecipitation buffer (0.1% SDS, 1% Triton X-100, 0.1% sodium deoxycholate, 140 mM NaCl,  $1\times$  protease inhibitors) and pre-cleared with 50  $\mu\text{l}$  GammaBind<sup>TM</sup> Plus Sepharose<sup>TM</sup> (Amersham Pharmacia Biotech), 20  $\mu\text{g}$  salmon sperm DNA, and 50  $\mu\text{g}$  BSA for 30 min at  $4^{\circ}\text{C}$ . Beads were pelleted and 10  $\mu\text{g}$  of antibody was added to supernatant and incubated overnight at  $4^{\circ}\text{C}$ . Immune complexes were collected with GammaBind<sup>TM</sup> Plus Sepharose<sup>TM</sup> and washed (Orlando *et al.*, 1997). DNA was eluted with 1% SDS, 0.1 M  $\text{NaHCO}_3$  for 15 min at room temperature. Crosslinks were reversed by incubating eluates at  $65^{\circ}\text{C}$  for 4 h in 0.2 M NaCl, followed by digestion with proteinase K (20  $\mu\text{g}$ ) in 10 mM EDTA, 40 mM Tris-HCl, pH 6.5 for 2 h at  $45^{\circ}\text{C}$ . DNA was recovered by phenol/chloroform/isoamyl alcohol extraction and ethanol precipitation. Specific AIB1 DNA was quantitated by real time PCR using the iCycler iQ Detection System (BioRad, Hercules, CA, USA). Amplification was performed in a 25  $\mu\text{l}$  final volume containing  $1\times$  reaction buffer (SYBR Green PCR core reagent kit, Applied Biosystems, Foster City, CA, USA) 3 mM  $\text{MgCl}_2$ , 0.25  $\mu\text{l}$  Platinum Taq polymerase (Life Technologies, Carlsbad, CA, USA), 0.2 mM dNTP, 2  $\mu\text{l}$  DNA a 1  $\mu\text{M}$  primers. The oligonucleotide primers used to detect AIB1 were 5'-AGCCGATGTATCTTCTACAGG-3' and 5'-AAAGCGGTCCTAAGGAGTCT-3'. The PCR reaction conditions were 10 min at  $95^{\circ}\text{C}$  followed by 50 cycles of 30 s each at  $95^{\circ}\text{C}$ ,  $58^{\circ}\text{C}$ , and  $72^{\circ}\text{C}$ . Fluorescent data were collected during the  $72^{\circ}\text{C}$  step. A dilution series of the plasmid pcDNA3-AIB1 was used as a standard.

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